

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 12:19:55 ; Search time 10.36 Seconds

(without alignments)
18.687 Million cell updates/sec

Title: US-09-759-484-3

Perfect score: 22

Sequence: 1 AMVSE 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	130	ANX1_CHICK	Q92108 gallus galli
2	22	100.0	202	BIN3_STAU	P20384 staphylococ
3	22	100.0	270	URED_ACPL	O54425 actinobacil
4	22	100.0	343	AN12_COLIT	Q92040 columba liv
5	22	100.0	343	ANX1_HUMAN	P04083 homo sapien
6	22	100.0	345	ANX1_MOUSE	P10107 mus musculu
7	22	100.0	345	ANX1_RAT	P07150 rattus norv
8	22	100.0	345	ANX1_RODSP	P24551 rodentia sp
9	22	100.0	346	ANX1_BOVIN	P46193 bos taurus
10	22	100.0	346	ANX1_PIG	P19619 sus scrofa
11	22	100.0	346	ANX1_RABIT	P51662 oryctolagus
12	22	100.0	379	HYPD_ALCEU	P31903 alcaligenes
13	22	100.0	395	NH10_CAEL	P41999 caenorhabdi
14	22	100.0	523	SRC_RSVA	P31693 rous sarcom
15	22	100.0	1862	GSAB_PICPA	Q94814 picchia past
16	22	95.5	148	REG2_PIRAB	Q94286 pyrococcus
17	22	95.5	279	F585_HABIN	P44018 haemophilus
18	22	95.5	543	CH62_SYNVU	O57002 synechococc
19	22	95.5	553	PRIS_DESVH	P31101 desulfobivr
20	22	95.5	576	Y065_CHLNV	Q92986 chlamydomo
21	22	95.5	1995	YCX7_CHIRE	P36495 chlamydomo
22	22	86.4	77	IM08_ARATH	Q93974 arabidopsis
23	22	86.4	90	LPB_HUMAN	O95969 homo sapien
24	22	86.4	131	SECR_PIG	P01279 sus scrofa
25	22	86.4	140	YQIB_ECOLI	P36652 escherichia
26	22	86.4	141	HBA1_HUMAN	P09109 homo sapien
27	22	86.4	161	VD14_HABIN	O57223 haemophilus
28	22	86.4	171	PHCB_SYNPW	P27289 synechococc
29	22	86.4	171	PHRE_SYNPZ	P11395 synechococc
30	22	86.4	181	Y065_CAEL	P34605 caenorhabdi
31	22	86.4	183	YMSJ_MARPO	P38471 marcanthia
32	22	86.4	187	VNSI_MOUSE	O62471 mus musculu
33	22	86.4	200	Y873_TREPA	O83843 treponema p

ALIGNMENTS

RESULT ID	1	ANX1_CHICK	STANDARD:	PRT:	130 AA.
AC	Q92108:	01-NOV-1997 (rel. 35, Created)			
DT	01-NOV-1997 (rel. 35, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)				
DE	(Phospholipase A2 inhibitory protein) (Fragment).				
GN	ANX1 OR ANX1				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=93374034; PubMed=8365470;				
RA	Sidls Y., Horseman N.D.;				
RT	"The hinge region of chicken annexin I contains no site for tyrosine phosphorylation.";				
RL	FEBS Lett. 329:296-300(1993).				
CC	-1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES				
CC	MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN				
CC	REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO				
CC	FOUR CALCIUM IONS WITH HIGH AFFINITY.				
CC	-1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS				
CC	SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS				
CC	MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.				
CC	-1- PHOSPHORYLATED BY PROTEIN KINASE C (BY SIMILARITY).				
CC	-1- POLYMORPHISM: IN CONTRAST TO PIGEON, CHICKEN CONTAINS NO ISOFORMS.				
CC	-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.				
CC	-----				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; S64951; AAB28036.2; -.				
DR	HSSP; P04083; 1B09.				
DR	InterPro; IPR001464; Annexin.				
DR	Pfam; PF00191; annexin; 1.				
DR	SMART; SMO0335; ANX; 1.				
DR	PROSITE; PS00223; ANNEXIN; 1.				
KW	Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;				
FT	Phospholipase A2 inhibitor.				
FT	REPEAT 46 106				
FT	ANNEXIN 1.				
FT	MOD_RES 118 >130				
FT	ANNEXIN 2.				
FT	MOD_RES 24 24				
FT	INTERCHAIN CROSS-LINK (BY SIMILARITY).				
FT	NON_TER 130 130				
FT	PHOSPHORYLATION (BY PKC) (BY SIMILARITY).				
SQ	SEQUENCE 130 AA; 14398 MW; 003AEF72F910551C CRC64;				

Query Match 100.0%; Score 22; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
 |||||
 DB 2 AMVSE 6

RESULT 2
 BIN1_STAU STANDARD: PRT: 202 AA.
 AC P20384;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Potential DNA-Invertase BIN3 (Transposon TN552).
 GN BIN3.
 OS Staphylococcus aureus.
 OG Plasmid p19789.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIC 9789;
 RX MEDLINE=90060039; PubMed=2555186;
 RA Rowland S.J.; Dyke K.G.H.;
 RT "Characterization of the staphylococcal beta-lactamase transposon
 RT Tn552.";
 RL EMO J. 8:2761-2773(1989).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RC STRAIN=NCIC 9789;
 RA Rowland S.J.;
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: BIN3 IS A POTENTIAL DNA INVERTASE.
 CC -1- SIMILARITY: BELONGS TO THE "RESOLVASE" FAMILY OF SITE-SPECIFIC
 CC RECOMBINASES.
 CC -----
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 CC -----
 CC EMBL: X16298; CAA34366.1; -
 CC PIR: S09385; S09385.
 DR HSSP: P03012; 2RSL.
 DR InterPro: IPR001822; Recombinase.
 DR Pfam: PF02796; HTH_7; 1.
 DR PROSITE: PS00397; RESOLVASE; 1.
 DR PROSITE: PS00398; RECOMBINASES_2; 1.
 KW Plasmid; Transposition; Transposable element; DNA recombination;
 KW DNA binding; DNA integration; DNA invertase.
 FT ACT_SITE 9
 FT TRANSIENT COVALENT LINKAGE TO DNA DURING
 FT STRAND CLEAVAGE AND REJOINING
 FT (BY SIMILARITY).
 FT
 SQ SEQUENCE 202 AA; 23360 MW; 7FB01DFE6102CE7 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
 |||||
 DB 118 AMVSE 122

RESULT 3
 URED_ACTPL STANDARD: PRT: 270 AA.
 ID URED_ACTPL
 AC 054425;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ured accessory protein ured.
 GN URED.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMS / SEROTYPE 1;
 RX MEDLINE=98013059; PubMed=9353010;
 RA Bosse J.T.; MacInnes J.I.;
 RT "Genetic and biochemical analyses of Actinobacillus pleuropneumoniae
 RT urease.";
 RL Infect. Immun. 65:4389-4394(1997).
 CC -1- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.
 CC -1- SIMILARITY: BELONGS TO THE URED FAMILY.
 CC -----
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 CC -----
 CC EMBL: U89957; AAC00065.1; -
 DR InterPro: IPR002669; Ured.
 DR Pfam: PF01774; Ured; 1.
 KW Nickel.
 SQ SEQUENCE 270 AA; 30215 MW; DB8C7F51D256B4B6 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 270;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
 |||||
 DB 213 AMVSE 217

RESULT 4
 AN12_COLLI STANDARD: PRT: 343 AA.
 ID AN12_COLLI
 AC 092040; O92041;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Anxin I, isoform P37 (Lipocortin I) (calpactin II) (Chromobindin 9)
 DE (Phospholipase A2 inhibitory protein).
 GN CP37.
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
 OX NCBI_TaxID=8932;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 13-50.
 RC STRAIN=WHITE CARRIEAU; TISSUE=Cropsac;
 RX MEDLINE=92406850; PubMed=1388165;
 RA Haigler H.T.; Mangili J.A.; Gao Y.; Jones J.; Horseman N.D.;
 RT "Identification and characterization of columbid anxin Icp37."
 RT Insights into the evolution of anxin I phosphorylation sites."
 RL J. Biol. Chem. 267:19123-19129(1992).
 RN [2]

RP SEQUENCE OF 1-154 FROM N.A.
RC STRAIN-N41; TISSUE-Liver;
RX MEDLINE-9426150; PubMed-8206371;
RA Gao Y., Horseman N.D.;
RT "Structural and functional divergences of the columbid annexin I-
RL encoding cp37 and cp35 genes.";
RL Gene 143:179-186(1994).
CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN
CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO
CC FOUR CALCIUM IONS WITH HIGH AFFINITY.
CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH
CC FACTOR RECEPTOR/KINASE.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- MISCELLANEOUS: IN PIGEONS, TWO ISOFORMS OF ANNEXIN-I ARE ENCODED
CC BY THE DIFFERENTIALLY REGULATED GENES CP35 AND CP37.
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -----
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CC -----
DR EMBL: M91008; AAA49447.1; ALT_INIT.
DR EMBL: L02504; AAA20674.1; -.
DR HSSP: P04083; 1B09.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin.4.
DR PRINTS: PR00196; ANNEXIN.
DR SMART: SM00335; ANX: 4.
DR PROSITE: PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat;
KW Phospholipase A2 inhibitor; Phosphorylation.
FT REPEAT 47 107
FT REPEAT 119 179
FT REPEAT 203 264
FT REPEAT 278 338
FT MOD_RES 19 19
FT MOD_RES 21 21
FT MOD_RES 24 24
FT CONFLICT 74 75
SQ SEQUENCE 343 AA; 38849 MW; 49A621A92BCDEPDC CRC64;

Query Match 100.0%; Score 22; DB 1; Length 343;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
| | | | |
DB 2 AMVSE 6

RESULT 5
ID ANX1_HUMAN STANDARD; PRT; 345 AA.
AC P04083;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)
DE (Phospholipase A2 inhibitory protein).
GN ANX1 OR ANX1 OR LPC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-86146879; PubMed-2936963;

RA Walner B.P., Mattaliano R.J., Hession C., Cate R.L., Tizard R.,
RA Sinclair L.K., Foeller C., Chow E.P., Browning J.L.,
RA Ramachandran K.L., Pepinsky R.B.;
RT "Cloning and expression of human lipocortin, a phospholipase A2
RT inhibitor with potential anti-inflammatory activity.";
RL Nature 320:77-81(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91369906; PubMed-1832554;
RA Kovacic R.T., Tizard R., Cate R.L., Frey A.Z., Walner B.P.;
RT "Correlation of gene and protein structure of rat and human
RT lipocortin I.";
RL Biochemistry 30:9015-9021(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-93145967; PubMed-8425544;
RA Arcote R., Arpaia G., Ruoppolo M., Malorni A., Pucci P., Marino G.,
RA Ialenti A., di Rosa M., Ciliberto G.;
RT "Structural characterization of a biologically active human
RT lipocortin I expressed in *Escherichia coli*.";
RL Eur. J. Biochem. 211:347-355(1993).
RN [4]
RP SEQUENCE, AND PHOSPHORYLATION SITES.
RX MEDLINE-88309771; PubMed-2457390;
RA Varticovski L., Chahwala S.B., Whitman M., Cantley L., Schindler D.,
RA Chow E.P., Sinclair L.K., Pepinsky R.B.;
RT "Location of sites in human lipocortin I that are phosphorylated by
RT protein tyrosine kinases and protein kinases A and C.";
RL Biochemistry 27:3682-3690(1988).
RN [5]
RP DIMERIC FORM.
RX MEDLINE-90104259; PubMed-2532504;
RA Pepinsky R.B., Sinclair L.K., Chow E.P., O'Brine-Greco B.;
RT "A dimeric form of lipocortin-1 in human placenta.";
RL Biochem. J. 263:97-103(1989).
RN [6]
RP ACETYLATION.
RX MEDLINE-87292145; PubMed-3303336;
RA Biemann K., Scoble H.A.;
RT "Characterization by tandem mass spectrometry of structural
RT modifications in proteins.";
RL Science 237:992-998(1987).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE-93200922; PubMed-8453382;
RA Weng X., Luecke H., Song I.S., Kang D.S., Kim S.-H., Huber R.;
RT "Crystal structure of human annexin I at 2.5-A resolution.";
RL Protein Sci. 2:448-458(1993).
RN [8]
RP STRUCTURE BY NMR OF 40-112.
RX MEDLINE-99115644; PubMed-9915835;
RA Gao J., Li Y., Yan H.;
RT "NMR solution structure of domain 1 of human annexin I shows an
RT autonomous folding unit.";
RL J. Biol. Chem. 274:2971-2977(1999).
CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN
CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO
CC FOUR CALCIUM IONS WITH HIGH AFFINITY.
CC -1- SUBUNIT: IN PLACENTA 20% OF THE PROTEIN IS FOUND AS A COVALENTLY
CC CROSS-LINKED DIMER WHICH IS GENERATED BY A TRANSGLUTAMINASE.
CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.
CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH
CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE
CC INHIBITORY ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- DATABASE: NAME-Annexin I home page;
CC WWW="http://www.mds.qmw.ac.uk/biopharm/ann1.html".
CC -----
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DR EMBL: X05908; CAA29338.1; -
DR PIR: A03080; LHM.
DR PIR: S28846; S28846.
DR PDB: 1AIN; 15-JUL-93.
DR PDB: 1BO9; 19-AUG-98.
DR PHCI-2DPAGE: P04083; -
DR MIM: 151690; -
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS: PR00196; ANNEXIN.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
KM Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure;
KW Phospholipase A2 inhibitor; Phosphorylation; Acetylation.
FT INIT_MET 0 0
FT REPEAT 50 110 ANNEXIN 1.
FT REPEAT 122 182 ANNEXIN 2.
FT REPEAT 206 266 ANNEXIN 3.
FT REPEAT 281 341 ANNEXIN 4.
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 18 1 INTERCHAIN CROSS-LINK.
FT MOD_RES 20 20 PHOSPHORYLATION (BY EGFR).
FT MOD_RES 23 23 PHOSPHORYLATION.
FT MOD_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SO SEQUENCE 345 AA; 38583 MW; 90A245C9B69F5011 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
Db 1 AMVSE 5

RESULT 6
ANXI_MOUSE STANDARD; PRT; 345 AA.
ID ANXI_MOUSE
AC P10107;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)
DE (Phospholipase A2 inhibitory protein).
GN ANXI OR ANXI OR LPC1 OR LPC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-DS;
RX MEDLINE=89098333; PubMed=2974946;
RA Sakata T., Iwagami S., Tsuruta Y., Suzuki R., Hojo K., Sato K.,
RA Teraoka H.;
RT "Mouse lipocortin I cDNA";
RL Nucleic Acids Res. 16:11818-11818(1988).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=91301692; PubMed=1676980;
RA Horlick K.R., Cheng I.C., Wong W.T., Wakeland E.K., Nick H.S.;
RT "Mouse lipocortin I gene structure and chromosomal assignment: gene
RL duplication and the origins of a gene family.";
RN Genomics 10:365-374(1991).
RN [3]
RN SEQUENCE OF 5-345 FROM N.A.

RX MEDLINE=89165848; PubMed=2522299;
RA Phillips C., Rose-John S., Rincke G., Fuerstenberger G., Marks F.;
RT "CDNA-cloning, sequencing and expression in glucocorticoid-stimulated
RT quiescent Swiss 3T3 fibroblasts of mouse lipocortin I.";
RL Biochem. Biophys. Res. Commun. 159:155-162(1989).

CC -I- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN
CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO
CC FOUR CALCIUM IONS WITH HIGH AFFINITY.
CC -I- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
CC MAY FORM ONE BINDING SITE FOR CALCIUM PROTEINS. A PAIR OF THESE REPEATS
CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE
CC INHIBITORY ACTIVITY (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

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DR EMBL: X07486; CAA30371.1; -
DR EMBL: M69260; AAA39437.1; -
DR EMBL: M69250; AAA39437.1; JOINED.
DR EMBL: M69251; AAA39437.1; JOINED.
DR EMBL: M69252; AAA39437.1; JOINED.
DR EMBL: M69253; AAA39437.1; JOINED.
DR EMBL: M69254; AAA39437.1; JOINED.
DR EMBL: M69255; AAA39437.1; JOINED.
DR EMBL: M69256; AAA39437.1; JOINED.
DR EMBL: M69257; AAA39437.1; JOINED.
DR EMBL: M69258; AAA39437.1; JOINED.
DR EMBL: M69259; AAA39437.1; JOINED.
DR EMBL: M24554; AAA39420.1; -
DR PIR: S02181; LUMS1.
DR HSSP: P04083; IBO9.
DR MGD: MGI:96819; Anx1.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS: PR00196; ANNEXIN.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat;
KW Phospholipase A2 inhibitor; Phosphorylation.
FT INIT_MET 0 0
FT REPEAT 50 110 ANNEXIN 1.
FT REPEAT 122 182 ANNEXIN 2.
FT REPEAT 206 266 ANNEXIN 3.
FT REPEAT 281 341 ANNEXIN 4.
FT MOD_RES 18 18 INTERCHAIN CROSS-LINK (BY SIMILARITY).
FT MOD_RES 20 20 PHOSPHORYLATION (BY EGFR).
FT MOD_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT CONFLICT 77 78 R -> I (IN REF. 2).
FT CONFLICT 211 211 R -> I (IN REF. 3).
FT CONFLICT 221 221 T -> H (IN REF. 3).
FT CONFLICT 273 273 T -> H (IN REF. 3).
SO SEQUENCE 345 AA; 38603 MW; 1785CADD691C3ED CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
Db 1 AMVSE 5

RESULT 7

ANX1_RAT
 ID ANX1_RAT STANDARD: PRT: 345 AA.
 AC P07150; 064664;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Annexin I (lipocortin I) (Calpactin II) (Chromobindin 9) (P35)
 DE (Phospholipase A2 inhibitory protein).
 GN ANX1 OR ANX1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=88015620; PubMed=2958780;
 RA Tanaka M., Nakamura E., Nishikubo C., Sakata T., Shin M., Teraoka H.;
 RT "Rat lipocortin I cDNA."
 RL Nucleic Acids Res. 15:7637-7637(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88284376; PubMed=2969352;
 RA Shimizu Y., Takabayashi E., Iano S., Shimizu N., Yamada K.,
 RA Gushima H.;
 RT "Molecular cloning and expression in Escherichia coli of the cDNA
 RT coding for rat lipocortin I (calpactin II)."
 RL Gene 65:141-147(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=91369906; PubMed=1832554;
 RA Kovacic R.T., Tizard R., Cate R.L., Frey A.Z., Wallner B.P.;
 RT "Correlation of gene and protein structure of rat and human
 RT lipocortin I."
 RL Biochemistry 30:9015-9021(1991).
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN
 CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO
 CC FOUR CALCIUM IONS WITH HIGH AFFINITY.
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
 CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
 CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH
 CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE
 CC INHIBITORY ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: Y00446; CAA68500.1; -
 DR EMBL: M19667; AAA40861.1; -
 DR EMBL: S57478; AAB19866.1; -
 DR EMBL: S57447; AAB19866.1; JOINED.
 DR EMBL: S57450; AAB19866.1; JOINED.
 DR EMBL: S57455; AAB19866.1; JOINED.
 DR EMBL: S57459; AAB19866.1; JOINED.
 DR EMBL: S57463; AAB19866.1; JOINED.
 DR EMBL: S57466; AAB19866.1; JOINED.
 DR EMBL: S57468; AAB19866.1; JOINED.
 DR EMBL: S57470; AAB19866.1; JOINED.
 DR EMBL: S57472; AAB19866.1; JOINED.
 DR EMBL: S57474; AAB19866.1; JOINED.
 DR EMBL: S57476; AAB19866.1; JOINED.
 DR PIR: JTD0303; LUR71.
 DR HSSP: P04083; LBO9.
 DR InterPro: IPR001464; Annexin.

DR Pfam: PF00191; annexin. 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR SMART: SM00335; ANX: 4.
 DR PROSITE: PS00223; ANNEXIN. 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat;
 KW Phospholipase A2 inhibitor; Phosphorylation.
 FT INIT_MET 0 0
 FT REPEAT 50 110 ANNEXIN 1.
 FT REPEAT 122 182 ANNEXIN 2.
 FT REPEAT 206 266 ANNEXIN 3.
 FT REPEAT 281 341 ANNEXIN 4.
 FT MOD_RES 18 18 INTERCHAIN CROSS-LINK (BY SIMILARITY).
 FT MOD_RES 20 20 PHOSPHORYLATION (BY EGFR) (BY
 FT SIMILARITY).
 FT MOD_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 FT FT 321 321 P -> S (IN REF. 3).
 FT CONFLICT 321 321
 SQ SEQUENCE 345 AA; 38698 MW; 74508E22527F224 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMYSE 5
 Db 1 AMYSE 5

RESULT 8
 ANX1_RAT
 ID ANX1_RAT STANDARD: PRT: 345 AA.
 AC P24551.
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Annexin I (lipocortin I) (Calpactin).
 GN ANX1 OR ANX1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; unclassified rodents.
 OX NCBI_TaxID=69158;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91054405; PubMed=2146952;
 RA Bobitzki A., Schroeder H.C., Ugarkovic D., Gramzow M., Fritsche U.,
 RA Babel R., Mueller W.E.G.;
 RT "cDNA structure and expression of calpactin, a peptide involved in
 RT Ca2(+)-dependent cell aggregation in sponges."
 RL Biochem. J. 271:415-420(1990).
 RN [2]
 RP DOUBT ON BIOLOGICAL SOURCE OF PROTEIN.
 RA Unpublished observations (FEB-1996).
 RN [3]
 RP AGREEMENT WITH RODENT CONTAMINATION.
 RA Mueller W.E.G.;
 RL Unpublished observations (APR-1996).
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS.
 CC -1- FUNCTION: AGGREGATION FACTOR (AF)-ASSOCIATED CALPACTIN AND PLASMA-
 CC MEMBRANE-BOUND PHOSPHOLIPIDS ARE INVOLVED IN CALCIUM-DEPENDENT
 CC CELL-CELL AGGREGATION IN SPONGES. CALPACTIN BINDS PHOSPHOLIPIDS.
 CC IT BINDS TWO CALCIUM IONS/MOL WITH LOW AFFINITY IN THE ABSENCE OF
 CC PHOSPHOLIPIDS, AND WITH HIGH AFFINITY IN THEIR PRESENCE.
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
 CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
 CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH
 CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE
 CC INHIBITORY ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- CAUTION: WAS THOUGHT TO ORIGINATE FROM THE SPONGE GEODIA CYDONIUM,
 CC BUT, ON THE BASIS OF PHYLOGENETIC STUDIES (REF.2), IT SEEMS

CC VERY PROBABLE THAT THE DNA SEQUENCE CODING FOR THIS PROTEIN COMES
 CC FROM A RODENT AS AGREED IN REF.3.

CC PIR: S13044; LUPL.
 CC HSSP: P04083; 1B09.
 CC InterPro: IPR001464; Annexin.
 CC Pfam: PF00191; annexin.4.
 CC PRINTS: PR00196; ANNEXIN.
 CC SMART: SM00335; ANX. 4.
 CC PROSITE: PS00223; ANNEXIN. 2.
 CC Annexin; Calcium/phospholipid-binding. Repeat; Phosphorylation.
 CC INIT_MET 0
 CC REPEAT 50 110 ANNEXIN 1.
 CC REPEAT 122 182 ANNEXIN 2.
 CC REPEAT 206 266 ANNEXIN 3.
 CC REPEAT 281 341 ANNEXIN 4.
 CC MOD_RES 18 18 INTERCHAIN CROSS-LINK (BY SIMILARITY).
 CC MOD_RES 20 20 PHOSPHORYLATION (BY EGFR) (BY
 CC SIMILARITY).
 CC MOD_RES 26 26 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 CC SEQUENCE 345 AA; 38921 MW; 1D856797F4DA0FFE CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMYSE 5
 11111
 DB 1 AMYSE 5

RESULT 9
 ANX1_BOVIN STANDARD; PRT; 346 AA.

ID ANX1_BOVIN
 AC P46193;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Annexin I (lipocortin I) (Calpactin II) (Chromobindin 9) (P35)
 DE (Phospholipase A2 inhibitory protein).
 GN ANX1 OR ANX1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93143727; PubMed=7678738;
 RA Ernst J.D.;
 RT "Epitope mapping of annexin I: antibodies that compete with
 phospholipids and calcium recognize amino acids 42-99.";
 RL Blochem. J. 289:539-542(1993).
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN
 REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO
 FOUR CALCIUM IONS WITH HIGH AFFINITY. BINDS MUSCLE ACTIN.
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
 SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
 MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.
 CC -1- PM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH
 FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE
 INHIBITORY ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: X56649; CA39971.1; -
 CC HSSP: P04083; 1B09.
 CC InterPro: IPR001464; Annexin.
 CC Pfam: PF00191; annexin.4.
 CC PRINTS: PR00196; ANNEXIN.
 CC SMART: SM00335; ANX. 4.
 CC PROSITE: PS00223; ANNEXIN. 3.
 CC Annexin; Calcium/phospholipid-binding. Repeat; Phosphorylation;
 CC Phospholipase A2 inhibitor.
 CC REPEAT 51 111 ANNEXIN 1.
 CC REPEAT 123 183 ANNEXIN 2.
 CC REPEAT 207 267 ANNEXIN 3.
 CC REPEAT 282 342 ANNEXIN 4.
 CC MOD_RES 19 19 INTERCHAIN CROSS-LINK (BY SIMILARITY).
 CC MOD_RES 21 21 PHOSPHORYLATION (BY EGFR) (BY
 CC SIMILARITY).
 CC MOD_RES 24 24 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 CC SEQUENCE 346 AA; 38897 MW; CD30701636DB23A7 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMYSE 5
 11111
 DB 2 AMYSE 6

RESULT 10
 ANX1_PIG

ID ANX1_PIG STANDARD; PRT; 346 AA.

AC P19619; 029547;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Annexin I (lipocortin I) (Calpactin II) (Chromobindin 9) (P35)
 DE (Phospholipase A2 inhibitory protein).
 GN ANX1 OR ANX1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE OF 6-346 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=97039680; PubMed=8885232;
 RA Seemann J., Weber K., Osborn M., Parton R.G., Gerke V.;
 RT "The association of annexin I with early endosomes is regulated by
 Ca2+ and requires an intact N-terminal domain.";
 RL Mol. Biol. Cell 7:1359-1374(1996).
 RN [2]
 RP SEQUENCE OF 13-42.
 RX MEDLINE=87008618; PubMed=3020049;
 RA De B.K., Misono K.S., Lukas T.J., Mroczkowski B., Cohen S.;
 RT "A calcium-dependent 35-kilodalton substrate for epidermal growth
 factor receptor/kinase isolated from normal tissue.";
 RL J. Biol. Chem. 261:13784-13792(1986).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=21103721; PubMed=11178908;
 RA Rosengarth A., Gerke V., Luecke H.;
 RT "X-ray structure of full-length annexin I and implications for
 membrane aggregation.";
 RL J. Mol. Biol. 306:489-498(2001).
 CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
 MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN
 REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO
 FOUR CALCIUM IONS WITH HIGH AFFINITY.
 CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
 SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
 MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.

CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH
CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE
CC INHIBITORY ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
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CC -----
CC EMBL: X95108; CAA64477.1; -
CC PIR: A26188; A26188.
CC PDB: 1HM6; 28-FEB-01.
CC InterPro: IPR001464; Annexin.
CC Pfam: PF00191; annexin; 4.
CC SMART: SM00335; ANX; 4.
CC PROSITE: PS00223; ANNEXIN; 3.
CC KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation; 3D-structure.
CC FT REPEAT 51 111 ANNEXIN 1.
CC FT REPEAT 123 183 ANNEXIN 2.
CC FT REPEAT 207 267 ANNEXIN 3.
CC FT REPEAT 282 342 ANNEXIN 4.
CC FT MOD.RES 19 19 INTERCHAIN CROSS-LINK (BY SIMILARITY).
CC FT MOD.RES 21 21 PHOSPHORYLATION (BY EGFR).
CC FT MOD.RES 24 24 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
CC FT CONFLICT 41 41 T -> S (IN REF. 2).
CC SQ SEQUENCE 346 AA; 38759 MW; 92584565DEBCAB2 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMYSE 5
Db 2 AMYSE 6
RESULT 11
ANX1_RABIT STANDARD; PRT; 346 AA.
AC P51662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Annexin I (Lipocortin I) (Calpactin II) (Chromobindin 9) (P35)
DE (Phospholipase A2 inhibitory protein).
GN ANX1 OR ANX1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Lung;
RA Tsao F.H.C.; Wen C.; Hu J.;
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
CC MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN
CC REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO
CC FOUR CALCIUM IONS WITH HIGH AFFINITY.
CC -1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.
CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH
CC FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE
CC INHIBITORY ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -----

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CC -----
CC EMBL: U24656; AAC78495.1; -
CC HSSP: P04083; 1B09.
CC InterPro: IPR001464; Annexin.
CC Pfam: PF00191; annexin; 4.
CC PRINTS: PR00196; ANNEXIN.
CC SMART: SM00335; ANX; 4.
CC PROSITE: PS00223; ANNEXIN; 3.
CC KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
CC Phospholipase A2 inhibitor.
CC FT REPEAT 51 111 ANNEXIN 1.
CC FT REPEAT 123 183 ANNEXIN 2.
CC FT REPEAT 207 267 ANNEXIN 3.
CC FT REPEAT 282 342 ANNEXIN 4.
CC FT MOD.RES 19 19 INTERCHAIN CROSS-LINK (BY SIMILARITY).
CC FT MOD.RES 21 21 PHOSPHORYLATION (BY EGFR) (BY
CC SIMILARITY).
CC FT MOD.RES 27 27 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
CC SQ SEQUENCE 346 AA; 38735 MW; 64EBDAF89D06A3D CRC64;

Query Match 100.0%; Score 22; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMYSE 5
Db 2 AMYSE 6
RESULT 12
HYPD_ALCEU STANDARD; PRT; 379 AA.
AC P31903;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hydropendin expression/formation protein hypd.
GN HYPD.
OS Alkaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H16 / ATCC 17699;
RA MEDLINE=93356597; PubMed=8352644;
RA Bernede J.; Eitinger M.; Friedrich B.;
RT Analysis of a pleiotropic gene region involved in formation of
RT catalytically active hydropendinases in Alkaligenes eutrophus H16.";
RL Arch. Microbiol. 159:545-553(1993).
CC -1- SIMILARITY: BELONGS TO THE HYPD FAMILY.
CC -----
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CC -----
CC EMBL: X70183; CAA49734.1; -
CC PIR: S29978; S29978.
CC InterPro: IPR002780; HYPD.
CC Pfam: PF01924; HYPD; 1.
CC -----

KW Metal-binding; Plasmid.
 FT METAL 64 POTENTIAL.
 FT METAL 67 POTENTIAL.
 SQ SEQUENCE 379 AA; 41907 MW; 510401FAAAGAB224 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 379;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
 DB 270 AMVSE 274

RESULT 13

NH10_CAEEL STANDARD; PRT; 395 AA.
 AC P41999;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Nuclear hormone receptor family member nhr-10.
 GN NHR-10 OR B0280.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Fulton L., Waterston R.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

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CC EMBL; U10438; AAA19086.1; -
 CC HSSP; P19793; 2NLL.
 DR WormPep; B0280.8; CE00815.
 DR InterPro; IPR000536; Hormone_rec_1lg.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00047; STR0IDFINGER.
 DR SMART; SM00430; HOL1.1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KM Zinc-finger.
 FT DNA_BIND 18 83 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 18 83 C4-TYPE.
 FT ZN_FING 54 78 C4-TYPE.
 SQ SEQUENCE 395 AA; 44899 MW; AFD8075D989EEBEA CRC64;

Query Match 100.0%; Score 22; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
 DB 119 AMVSE 123

RESULT 14

SRC_RSVP STANDARD; PRT; 523 AA.
 ID SRC_RSVP
 AC P31693;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein SRC (EC 2.7.1.112) (P60-SRC).
 DE SRC.
 GN V-SRC.
 OS Rous sarcoma virus (strain PA101T).
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID=31667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92351554; PubMed=1322589;
 RA Dazelaar P., Barnier J.V., Hampe A., Laugier D., Marx M., Galibert F.,
 RA Calothy G.;
 RT "Small deletion in v-src SH3 domain of a transformation defective
 RT mutant of Rous sarcoma virus restores wild type transforming
 RT properties.";
 RL Virology 189:556-567(1992).

CC -1- FUNCTION: THIS PHOSPHOPROTEIN. REQUIRED FOR BOTH THE INITIATION
 CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
 CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
 CC IN VITRO.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SRC SUBFAMILY.

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CC EMBL; M64475; AAA42581.1; ALT_SEQ.
 DR PIR; A42994; TFEVMT.
 DR HSSP; P00524; ISPS.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;
 KW ATP-binding; Myristate; SH3 domain; SH2 domain.
 FT LIPID 2 MYRISTATE.
 FT DOMAIN 75 139 SH3.
 FT DOMAIN 145 242 SH2.
 FT DOMAIN 264 514 PROTEIN KINASE.
 FT NP_BIND 270 278 ATP (BY SIMILARITY).
 FT BINDING 292 292 ATP (BY SIMILARITY).
 FT ACT_SITE 383 383 BY SIMILARITY.
 FT MOD_RES 413 413 PHOSPHORYLATION (AUTO-).
 SQ SEQUENCE 523 AA; 58778 MW; 853245739F6B90ED CRC64;

